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PATENT

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

STEPHEN M. ALLEN ET AL.

CASE NO.: BB1429 US NA

APPLICATION NO.: 09/740,288

GROUP ART UNIT: 1652

FILED: DECEMBER 19, 2000

EXAMINER: M. WALICKA

CONFIRMATION NO.: 8577

FOR: PLANT BIOTIN SYNTHASE

RECEIVED

OCT 30 2002

AMENDMENT AND RESPONSE UNDER 37 C.F.R. § 1.111

TECH CENTER 1600/290

Commissioner of Patents and Trademarks  
Washington, D.C. 20231

Sir:

This is in response to the Office Action Dated April 23, 2002, regarding the above-identified application. Reconsideration is respectfully requested and the following submitted in support thereof.

**IN THE SPECIFICATION:**

Please replace paragraph on page 9, lines 6-28, with the following:

p1  
A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence.